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**AP Biology Lab #1: Modeling Hardy-Weinberg Equilibrium**

Ms. Ottolini, 2013-2014

***Directions:*** In this lab, you will be tracking allele, genotype, and phenotype frequencies for the trait of “color” in a population. By analyzing these frequencies in your individual data and the class data, you will be able to determine whether a population is in Hardy Weinberg Equilibrium.

There are two parts to the simulation. In the first part, you will be modeling an “ideal” population in Hardy Weinberg Equilibrium. In the second part, you will be modeling a population that is undergoing natural selection to favor a particular color.

As you progress through the lab, answer all associated lab questions. These questions will not be graded, but they will help you prepare your “mini lab report,” which will consist of a modified introduction section and discussion section. Since you will not be creating a hypothesis and designing the experiment, the rubric for this “mini lab report” will be slightly different from the normal lab report rubric for this class. The rubric is given at the end of this packet.

**Case #1: A Test of the Ideal Hardy-Weinberg Population**

In this case, the whole class will represent a breeding population. As an “ideal” case, we will try

to maintain the five Hardy-Weinberg conditions that would keep allele frequencies the same

from generation to generation. To model random mating, students must choose another student

as a mate at random. In this simulation, neither sex (male or female) nor genotype influences

mate selection.

1. As the breeding population, the class will start out with an equal percentage of dominant and

recessive alleles in the gene pool. To simulate this all individuals will start out as

**heterozygotes** (*Aa*).

2. As heterozygotes, each individual will be given a cup with two *A* alleles (2 black chips) and

two *a* alleles (2 white chips). Honestly, this confused me the first time I read it, but the reason you have 4 alleles rather than 2 for this trait is that right before meiosis, replication occurs to give you two copies of each chromosome and allele. So you should have two A’s and two a’s. These alleles (chips) represent the alleles found in the gametes produced during meiosis. (Remember meiosis produces 4 gametes.) When mating each “parent” contributes one of these alleles to their offspring.

3. To mate and produce an offspring, each “parent” will select a gamete out of their mate’s

cup. Put these two gametes together (fertilization) to make an offspring with two copies of the allele. Only one of the parents records this genotype as their offspring in the Data Table below.

4. Each parental pair, must produce two offspring, so the gametes (chips) must be returned to

the original cups, so a second pair of gametes can produce a second offspring in the same

manner. Only the other parent then records the genotype of their offspring in the Data Table.

5. This generation has now reproduced, and as with many organisms, after reproduction these

parents *senesce* and die. The two student partners will now become the next generation by

assuming the genotypes of the *two offspring* they just produced.

6. Each student should obtain, if necessary, new chips representing the alleles that would be

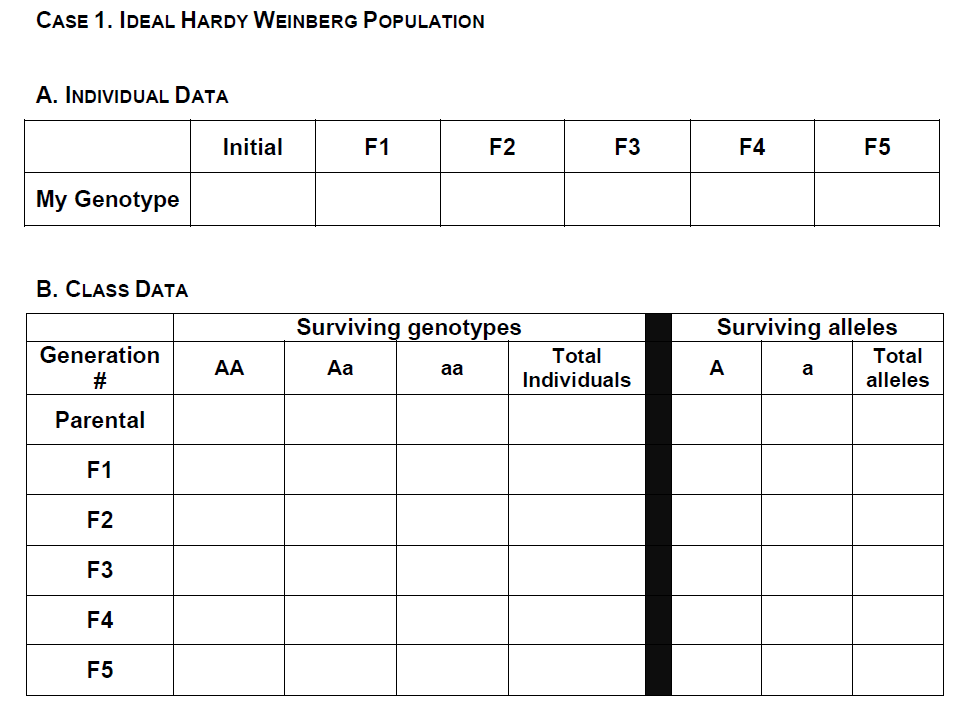
produced from meiosis in this new individual. For example, if you are now *aa*, then your

gametes would be *a*, *a*, *a*, *a* and you would place 4 white chips in your cup.)

7. Each student should now seek out a *new mate* at random from the other individuals in the

classroom. Remember the sex and genotype of your classmates should be disregarded.

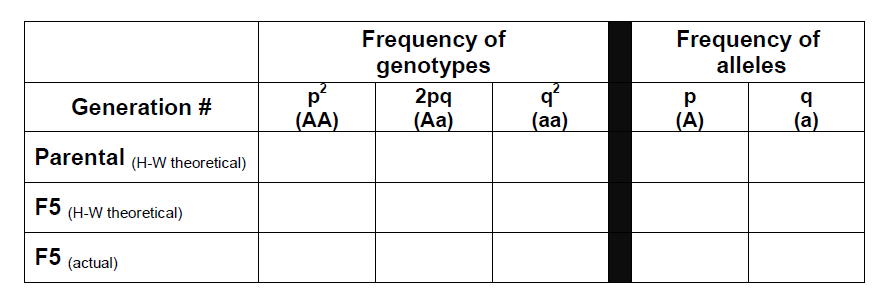
8. Pool class data for data analysis.



9. Complete the table below: For the population (class data), what are the **theoretical allele &**

**genotype frequencies** in the initial parental generation? Based on the Hardy-Weinberg

theorem, what would the **theoretical allele & genotype frequencies** be for the 5th generation? What are the **actual allele & genotype frequencies** at the end of the 5th generation?



10. *Run a Chi square test on your generation F5 genotype frequency results using the Chi Square tutorial document reviewed in class. This test will allow you to determine whether your results match with what you would expect for a population in Hardy-Weinberg equilibrium.*

**Case #2: Selection Against the Homozygous Recessive Genotype**

In the natural world, not all genotypes have the same rates of survival. The environment may

favor some genotypes while selecting against others. In Case 2, we will create a more realistic

simulation by applying a selection pressure to the population. In this Case, you will assume that

the homozygous recessive individuals never survive (100% selection against), and that

heterozygous and homozygous dominant individuals survive 100% of the time.

13. Start again with your initial heterozygote genotype (2 white chips & 2 black chips). Produce

your “offspring” as you did in Case 1. This time however, if your offspring is *aa* it does not

survive to reproduce. Since we want to maintain a constant population size, the same two

parents must try again until they produce two surviving offspring. Record your surviving

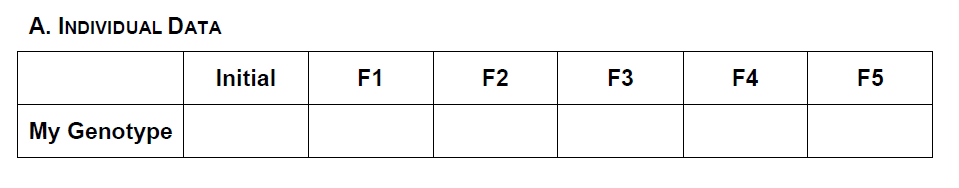
offspring in the Data Table below.

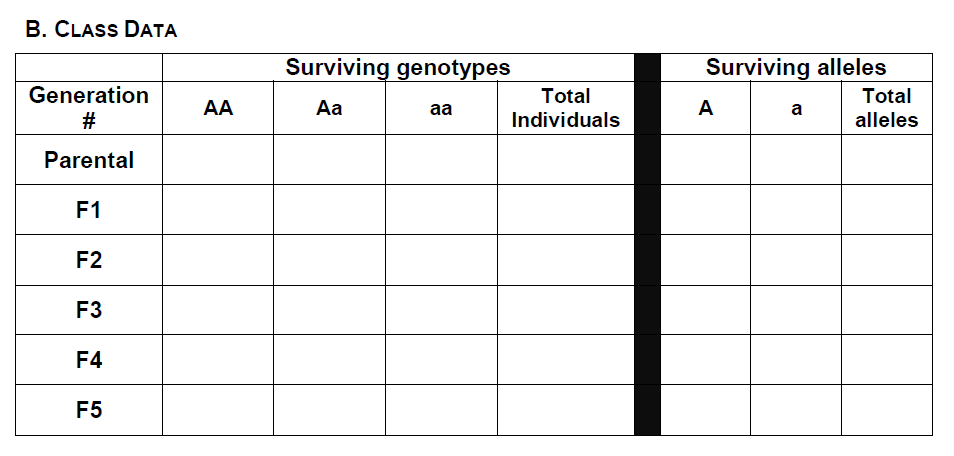
14. As in Case 1, after successfully reproducing, you become your surviving offspring and mate

at random with another individual in the population. Record the genotype of your offspring in

the Data Table below.

15. Pool class data for data analysis.





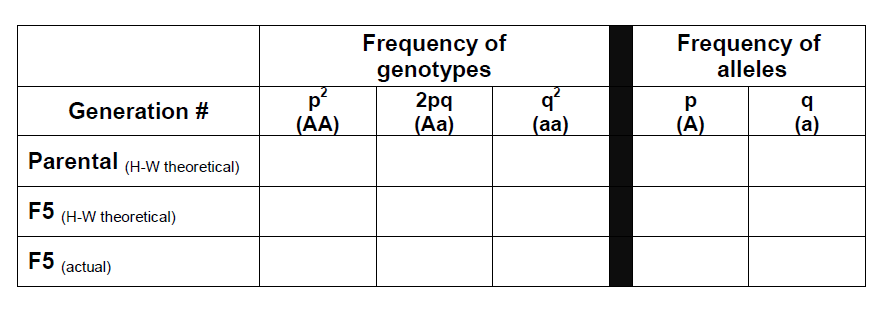
16. Complete the table below: For the population (class data), what are the **theoretical allele &**

**genotype frequencies** in the initial parental generation? Based on the Hardy-Weinberg

theorem, what would the **theoretical allele & genotype frequencies** be for the 5th

generation? What are the **actual allele & genotype frequencies** at the end of the 5th

generation?



17. *Run a Chi square test on your generation F5 genotype frequency results using the Chi Square tutorial document reviewed in class. This test will allow you to determine whether your results match with what you would expect for a population in Hardy-Weinberg equilibrium.*

18. Predict what would happen to the p and q frequencies if you simulated another five

generations.

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19. Since homozygous recessives are strongly selected against, would you expect the

recessive (a) allele to be completely removed from the population? In other words, in a large

population would it be possible to completely eliminate a deleterious (or even lethal)

recessive allele. Explain.

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**Writing Your Mini Lab Report:**

***Directions:*** You will be including an introduction section and a discussion/conclusion section in this mini lab report. You mini lab report should be titled “Mini Lab Report: Hardy Weinberg Equilibrium Simulation.” This report should be typed, 12 point font, and double spaced. Make sure to include your name, date, and class period at the top right corner of the page. Please include “introduction” and “discussion / conclusion” subtitles so that I know which sections are which. You may find that you need more than one paragraph to fully meet the requirements for each section. Please detach this page and staple it to your completed lab report. You will have two grades in the grade book. There will be one grade for the introduction section (weighted as 57% of the assignment) and one grade for the discussion/ conclusion section (weighted as 43% of the assignment)

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| **Section** | **Criteria** | **Point Breakdown** | **Total Grade** |
| Introduction  *(Science Practice 3)* | A. The introduction thoroughly explains what the Hardy Weinberg equations are intended to model  B. The introduction identifies and explains the meaning of all terms in the Hardy-Weinberg equations (i.e. p, q, p2, 2pq, and q2)  C. The introduction identifies the five conditions that a population must meet to be in Hardy Weinberg Equilibrium  D. The introduction clearly and accurately outlines how and why the set-up of Case #1 is different from Case #2.  E. The introduction identifies and explains the Null hypothesis, which forms the basis of our later X2 test comparing the class genotype results with the expected results for a population in Hardy Weinberg equilibrium  *(Note: the Null hypothesis should be the same for Case #1 and Case #2)*  F. The introduction clearly explains why we use the entire class’s data rather than one group’s data to draw conclusions. | /2 | **\_\_\_\_/13 = \_\_\_\_%** |
| /4 |
| /2 |
| /2 |
| /2 |
| /1 |
| Discussion and Conclusion  *(Science Practice 5)* | A. There is a thorough and accurate explanation/analysis of how the class genotype results in Case #1 relate back to our expected genotype frequencies for a population in Hardy Weinberg Equilibrium  *(Note: You must discuss your X2 test results for Case #1 when comparing your class data to your expected values)*  B. There is a thorough and accurate explanation/analysis of how the class genotype results in Case #2 relate back to our expected genotype frequencies for a population in Hardy Weinberg Equilibrium  *(Note: You must discuss your X2 test results for Case #2 when comparing your class data to your expected values)*  C. There is a thorough and accurate discussion of Question #18 and #19 (restated below).  “How will p and q frequencies continue to change, and will the recessive allele ever be completely eliminated from the population?” | /4 | **\_\_\_\_/10 = \_\_\_\_%** |
| /4 |
| /2 |

***Rubric:***

***Teacher Comments:***